

Database : UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query				Description
No.	Score	Match	Length	DB	ID
1	925	54.2	322	1	ALDX_SPOSA
2	658	38.5	315	2	Q9AW93
3	654	38.3	323	2	Q6C177
4	653	38.2	315	2	Q9AW92
5	651.5	38.1	316	2	Q9VTK9
6	648.5	38.0	324	1	AKA1_RAT
7	647	37.9	312	1	GCY_YEAST
8	640.5	37.5	324	1	AKA1_MOUSE
9	640.5	37.5	325	2	Q80XJ7
10	639.5	37.4	313	2	O82020
11	638	37.4	350	2	Q8IQF8
12	636.5	37.3	324	1	AKA1_PIG
13	635.5	37.2	324	1	AKA1_HUMAN
14	634	37.1	327	2	P74308
15	631.5	37.0	324	2	Q6AZW2
16	631.5	37.0	327	2	Q6GMC7
17	627	36.7	290	2	O80945
18	623	36.5	314	2	Q84TF0
19	621.5	36.4	311	2	Q941T6
20	621.5	36.4	350	2	Q7XJP3
21	620	36.3	312	1	YPR1_YEAST
22	618	36.2	304	2	Q84W94
23	616.5	36.1	327	2	Q6AZC3
24	614.5	36.0	311	2	Q941T8

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	925	54.2	323	2	S78113	aldehyde reductase
2	648.5	38.0	325	1	JN0629	alcohol dehydrogen
3	647	37.9	312	1	S22846	probable aldehyde
4	639.5	37.4	313	2	T09670	abscisic acid acti
5	635.5	37.2	325	2	A33851	alcohol dehydrogen
6	634	37.1	327	1	S76143	probable aldehyde
7	627	36.7	290	2	T02543	aldehyde dehydroge
8	621.5	36.4	350	2	B84797	probable alcohol d
9	620	36.3	312	2	S61163	aldo-keto reductas
10	610.5	35.7	316	2	T26766	hypothetical prote
11	609	35.7	315	2	T45928	reductase-like pro
12	603.5	35.3	321	2	T38413	probable oxidoredu
13	599.5	35.1	316	1	A60603	aldehyde reductase
14	591.5	34.6	316	1	A39763	aldehyde reductase
15	585.5	34.3	315	1	A35452	aldehyde reductase
16	585.5	34.3	316	2	I49484	aldehyde reductase
17	575.5	33.7	316	2	A59021	aldehyde reductase
18	573.5	33.6	323	2	JC5240	3alpha-hydroxychol
19	573	33.5	294	2	T02542	probable alcohol d

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
1	1708	100.0	328	13	US-10-040-416-4	Sequence 4, Appli
2	1697	99.4	328	13	US-10-040-416-6	Sequence 6, Appli
3	1495	87.5	330	9	US-09-800-487A-2	Sequence 2, Appli
4	1495	87.5	330	13	US-10-040-416-2	Sequence 2, Appli
5	906.5	53.1	322	10	US-09-734-237B-32	Sequence 32, Appli
6	684.5	40.1	356	15	US-10-369-493-13122	Sequence 13122, A
7	673.5	39.4	313	15	US-10-424-599-221377	Sequence 221377,
8	668	39.1	313	15	US-10-424-599-282510	Sequence 282510,
9	660	38.6	314	15	US-10-424-599-144593	Sequence 144593,
10	656	38.4	298	15	US-10-369-493-13144	Sequence 13144, A
11	650	38.1	313	10	US-09-882-691-6	Sequence 6, Appli
12	650	38.1	313	15	US-10-424-599-221378	Sequence 221378,
13	648.5	38.0	325	16	US-10-472-317-36	Sequence 36, Appli
14	647	37.9	312	10	US-09-734-237B-42	Sequence 42, Appli
15	647	37.9	312	15	US-10-369-493-22372	Sequence 22372, A

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query				Description
	Score	Match	Length	DB	
1	906.5	53.1	322	4	US-09-734-237B-32 Sequence 32, Appl
2	650	38.1	313	3	US-09-347-803-6 Sequence 6, Appl
3	647	37.9	312	4	US-09-734-237B-42 Sequence 42, Appl
4	647	37.9	313	4	US-09-734-237B-44 Sequence 44, Appl
5	639.5	37.4	313	3	US-09-347-803-25 Sequence 25, Appl
6	620	36.3	313	4	US-09-734-237B-39 Sequence 39, Appl
7	608.5	35.6	308	3	US-09-347-803-8 Sequence 8, Appl
8	600.5	35.2	302	4	US-09-270-767-45294 Sequence 45294, A
9	599.5	35.1	316	3	US-08-801-344-4 Sequence 4, Appl
10	599.5	35.1	316	3	US-09-498-599-4 Sequence 4, Appl
11	584	34.2	290	4	US-09-248-796A-17316 Sequence 17316, A
12	574.5	33.6	316	1	US-08-585-595-3 Sequence 3, Appl

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	1708	100.0	328	5	ABP53551	Abp53551 T. megach
2	1697	99.4	328	5	ABP53552	Abp53552 T. megach
3	1495	87.5	330	5	ABP53550	Abp53550 T. megach
4	925	54.2	323	2	AAR96294	Aar96294 Carbonyl
5	906.5	53.1	322	4	AAG63561	Aag63561 Amino aci
6	684.5	40.1	356	8	ADS24089	Ads24089 Bacterial
7	656	38.4	298	8	ADS24111	Ads24111 Bacterial
8	650	38.1	313	4	AAB47466	Aab47466 G. max al
9	650	38.1	313	7	AAE39522	Aae39522 Soybean a
10	648.5	38.0	325	5	ABP53620	Abp53620 Glucurona
11	648.5	38.0	325	8	ADF42772	Adf42772 Rat aldeh
12	648	37.9	312	2	AAW29218	Aaw29218 S. cerevi
13	647.5	37.9	313	2	AAY06231	Aay06231 Alfalfa a

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_htc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	234.8	21.8	790	7	CF642818	CF642818 D56_C10 F
2	225	20.9	706	7	CF644498	CF644498 K21_H01 F
3	206.6	19.2	1061	4	BI948347	BI948347 HVSME1000
4	186	17.3	585	7	CF638990	CF638990 D09_H04 F
5	184	17.1	556	6	CD489982	CD489982 T30_H09 T
6	184	17.1	619	7	CF643073	CF643073 D59_D08 F
7	183	17.0	551	7	CF639302	CF639302 D13_H10 F
8	179.8	16.7	547	7	CV096678	CV096678 FAMU_USDA
9	179.4	16.7	684	7	CK447487	CK447487 N1A12.SP6
10	169.2	15.7	687	7	CK447233	CK447233 N7C2.SP6
11	167.6	15.6	626	6	CD488246	CD488246 T06_E03 T
12	163.6	15.2	779	1	AA263299	AA263299 LD06393.5
13	163.4	15.2	510	7	CF639847	CF639847 D20_D06 F
14	162.6	15.1	758	1	AA697426	AA697426 HL02448.5
15	161.8	15.0	477	7	CF640529	CF640529 D28_D04 F
16	161.4	15.0	638	6	CA015279	CA015279 HT13N05r
17	160.8	14.9	769	7	CF869025	CF869025 tric017xh
18	160.8	14.9	823	6	CB899137	CB899137 tric017xh
19	160.4	14.9	746	7	CV528275	CV528275 dba59b08.
20	159.6	14.8	384	7	CF640582	CF640582 D28_H11 F

Database : Published\_Applications\_NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*

12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*

13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*

14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*

15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*

16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*

17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*

18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*

19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*

20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*

21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
<hr/>						
1	1077	100.0	1077	13	US-10-040-416-3	Sequence 3, Appli
2	1040.2	96.6	1121	13	US-10-040-416-5	Sequence 5, Appli
3	613.4	57.0	1119	9	US-09-800-487A-1	Sequence 1, Appli
4	613.4	57.0	1119	13	US-10-040-416-1	Sequence 1, Appli
5	315.4	29.3	972	10	US-09-734-237B-31	Sequence 31, Appli
6	279.4	25.9	972	10	US-09-734-237B-33	Sequence 33, Appli

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query				Description
	Score	Match	Length	DB ID	
1	315.4	29.3	972	4 US-09-734-237B-31	Sequence 31, Appl
2	279.4	25.9	972	4 US-09-734-237B-33	Sequence 33, Appl
3	155.6	14.4	954	2 US-08-336-198C-2	Sequence 2, Appl
4	155.6	14.4	954	4 US-09-184-965-2	Sequence 2, Appl
5	154.2	14.3	1290	4 US-09-270-767-13724	Sequence 13724, A
6	148.8	13.8	1073	3 US-09-347-803-5	Sequence 5, Appl
7	143.2	13.3	1512	4 US-09-270-767-15148	Sequence 15148, A
8	143	13.3	1337	3 US-08-801-344-3	Sequence 3, Appl
9	143	13.3	1337	3 US-09-498-599-3	Sequence 3, Appl
10	136	12.6	1132	4 US-09-626-002-18	Sequence 18, Appl
11	128.4	11.9	1335	4 US-09-023-655-1010	Sequence 1010, Ap
12	124	11.5	1196	4 US-09-626-002-17	Sequence 17, Appl
13	121.6	11.3	942	4 US-09-734-237B-43	Sequence 43, Appl
14	117	10.9	942	4 US-09-734-237B-40	Sequence 40, Appl

Database : N\_Geneseq\_16Dec04:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1077	100.0	1077	6	ABQ82226	Abq82226 T. megach
2	1040.2	96.6	1121	6	ABQ82227	Abq82227 T. megach
3	613.4	57.0	1119	6	ABQ82225	Abq82225 T. megach
4	315.4	29.3	972	2	AAT29160	Aat29160 Carbonyl
5	315.4	29.3	972	5	AAH74577	Aah74577 Nucleotid
6	315.4	29.3	1055	2	AAT29159	Aat29159 Carbonyl
7	279.4	25.9	972	5	AAH74578	Aah74578 A synthet
8	180.4	16.8	656	8	ABZ53102	Abz53102 Aspergill
9	163.6	15.2	978	4	ABL10491	Ab110491 Drosophil
10	157.2	14.6	1231	2	AAX58867	Aax58867 Alfalfa a
11	155.6	14.4	954	2	AAQ14352	Aaq14352 Xylose re

Database : GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	1077	100.0	1077	6	BD177580	BD177580 Erythrose
2	1077	100.0	1077	6	BD177585	BD177585 Erythrose
3	1077	100.0	1077	6	AX470402	AX470402 Sequence
4	1040.2	96.6	1121	6	BD177581	BD177581 Erythrose
5	1040.2	96.6	1121	6	BD177586	BD177586 Erythrose
6	1040.2	96.6	1121	6	AX470403	AX470403 Sequence
7	613.4	57.0	1119	6	BD177579	BD177579 Erythrose
8	613.4	57.0	1119	6	BD177584	BD177584 Erythrose
9	613.4	57.0	1119	6	AX470401	AX470401 Sequence
10	315.4	29.3	1055	6	E11242	E11242 cDNA encodi
11	170.6	15.8	2309	8	SSU26463	U26463 Sporidiobol
12	163.6	15.2	978	6	CQ585219	CQ585219 Sequence